#5

SEQUENCE LISTING

<110> RIEPING, MECHTHILD
BASTUCK, CHRISTINE
HERMANN, THOMAS
THIERBACH, GEORG

<120> FERMENTATIVE PROCESS FOR THE PREPARATION OF L-AMINO ACIDS
USING STRAINS OF THE FAMILY ENTEROBACTERIACEAE

<130> 21123/283665/MAS

<140> 09/963,668
<141> 2001-09-27

<150> DE 100 48 605.3
<151> 2000-09-30

<150> DE 100 55 516.0
<151> 2000-11-09

<150> DE 101 30 192.8
<151> 2001-06-22

<160> 19

<170> PatentIn Ver. 2.1

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atc agt gac gta cat gat atc gtt tac aac cca agc tac gac ctg ctg 96
Ile Ser Asp Val His Asp Ile Val Tyr Asn Pro Ser Tyr Asp Leu Leu
20 25 30

tat cag gaa gag ctc gat ccg agc ctg aca ggt tat gag cgc ggg gtg 144
Tyr Gln Glu Glu Leu Asp Pro Ser Leu Thr Gly Tyr Glu Arg Gly Val
35 40 45

tta act aat ctg ggt gcc gtt gcc gtc gat acc ggg atc ttc acc ggt 192
Leu Thr Asn Leu Gly Ala Val Ala Val Asp Thr Gly Ile Phe Thr Gly
50 55 60

cgt tca cca aaa gat aag tat atc gtc cgt gac gat acc act cgc gat 240
Arg Ser Pro Lys Asp Lys Tyr Ile Val Arg Asp Asp Thr Thr Arg Asp
65 70 75 80

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act ttc tgg tgg gca gac aaa ggc aaa ggt aag aac gac aac aaa cct     288
Thr Phe Trp Trp Ala Asp Lys Gly Lys Gly Lys Asn Asp Asn Lys Pro
                 85                  90                  95

ctc tct ccg gaa acc tgg cag cat ctg aaa ggc ctg gtg acc agg cag     336
Leu Ser Pro Glu Thr Trp Gln His Leu Lys Gly Leu Val Thr Arg Gln
            100                 105                 110

ctt tcc ggc aaa cgt ctg ttc gtt gtc gac gct ttc tgt ggt gcg aac     384
Leu Ser Gly Lys Arg Leu Phe Val Val Asp Ala Phe Cys Gly Ala Asn
        115                 120                 125

ccg gat act cgt ctt tcc gtc cgt ttc atc acc gaa gtg gcc tgg cag     432
Pro Asp Thr Arg Leu Ser Val Arg Phe Ile Thr Glu Val Ala Trp Gln
    130                 135                 140

gcg cat ttt gtc aaa aac atg ttt att cgc ccg agc gat gaa gaa ctg     480
Ala His Phe Val Lys Asn Met Phe Ile Arg Pro Ser Asp Glu Glu Leu
145                 150                 155                 160

gca ggt ttc aaa cca gac ttt atc gtt atg aac ggc gcg aag tgc act     528
Ala Gly Phe Lys Pro Asp Phe Ile Val Met Asn Gly Ala Lys Cys Thr
                165                 170                 175

aac ccg cag tgg aaa gaa cag ggt ctc aac tcc gaa aac ttc gtg gcg     576
Asn Pro Gln Trp Lys Glu Gln Gly Leu Asn Ser Glu Asn Phe Val Ala
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ttt aac ctg acc gag cgc atg cag ctg att ggc ggc acc tgg tac ggc     624
Phe Asn Leu Thr Glu Arg Met Gln Leu Ile Gly Gly Thr Trp Tyr Gly
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ggc gaa atg aag aaa ggg atg ttc tcg atg atg aac tac ctg ctg ccg     672
Gly Glu Met Lys Lys Gly Met Phe Ser Met Met Asn Tyr Leu Leu Pro
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ctg aaa ggt atc gct tct atg cac tgc tcc gcc aac gtt ggt gag aaa     720
Leu Lys Gly Ile Ala Ser Met His Cys Ser Ala Asn Val Gly Glu Lys
225                 230                 235                 240

ggc gat gtt gcg gtg ttc ttc ggc ctt tcc ggc acc ggt aaa acc acc     768
Gly Asp Val Ala Val Phe Phe Gly Leu Ser Gly Thr Gly Lys Thr Thr
                245                 250                 255

ctt tcc acc gac ccg aaa cgt cgc ctg att ggc gat gac gaa cac ggc     816
Leu Ser Thr Asp Pro Lys Arg Arg Leu Ile Gly Asp Asp Glu His Gly
            260                 265                 270

tgg gac gat gac ggc gtg ttt aac ttc gaa ggc ggc tgc tac gca aaa     864
Trp Asp Asp Asp Gly Val Phe Asn Phe Glu Gly Gly Cys Tyr Ala Lys
        275                 280                 285

act atc aag ctg tcg aaa gaa gcg gaa cct gaa atc tac aac gct atc     912
Thr Ile Lys Leu Ser Lys Glu Ala Glu Pro Glu Ile Tyr Asn Ala Ile
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cgt cgt gat gcg ttg ctg gaa aac gtc acc gtg cgt gaa gat ggc act    960
Arg Arg Asp Ala Leu Leu Glu Asn Val Thr Val Arg Glu Asp Gly Thr
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atc gac ttt gat gat ggt tca aaa acc gag aac acc cgc gtt tct tat   1008
Ile Asp Phe Asp Asp Gly Ser Lys Thr Glu Asn Thr Arg Val Ser Tyr
                325                 330                 335

ccg atc tat cac atc gat aac att gtt aag ccg gtt tcc aaa gcg ggc   1056
Pro Ile Tyr His Ile Asp Asn Ile Val Lys Pro Val Ser Lys Ala Gly
            340                 345                 350

cac gcg act aag gtt atc ttc ctg act gct gat gct ttc ggc gtg ttg   1104
His Ala Thr Lys Val Ile Phe Leu Thr Ala Asp Ala Phe Gly Val Leu
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ccg ccg gtt tct cgc ctg act gcc gat caa acc cag tat cac ttc ctc   1152
Pro Pro Val Ser Arg Leu Thr Ala Asp Gln Thr Gln Tyr His Phe Leu
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tct ggc ttc acc gcc aaa ctg gcc ggt act gag cgt ggc atc acc gaa   1200
Ser Gly Phe Thr Ala Lys Leu Ala Gly Thr Glu Arg Gly Ile Thr Glu
385                 390                 395                 400

ccg acg cca acc ttc tcc gct tgc ttc ggc gcg gca ttc ctg tcg ctg   1248
Pro Thr Pro Thr Phe Ser Ala Cys Phe Gly Ala Ala Phe Leu Ser Leu
                405                 410                 415

cac ccg act cag tac gca gaa gtg ctg gtg aaa cgt atg cag gcg gcg   1296
His Pro Thr Gln Tyr Ala Glu Val Leu Val Lys Arg Met Gln Ala Ala
            420                 425                 430

ggc gcg cag gct tat ctg gtt aac act ggc tgg aac ggc act ggc aaa   1344
Gly Ala Gln Ala Tyr Leu Val Asn Thr Gly Trp Asn Gly Thr Gly Lys
        435                 440                 445

cgt atc tcg att aaa gat acc cgc gcc att atc gac gcc atc ctc aac   1392
Arg Ile Ser Ile Lys Asp Thr Arg Ala Ile Ile Asp Ala Ile Leu Asn
    450                 455                 460

ggt tcg ctg gat aat gca gaa acc ttc act ctg ccg atg ttt aac ctg   1440
Gly Ser Leu Asp Asn Ala Glu Thr Phe Thr Leu Pro Met Phe Asn Leu
465                 470                 475                 480

gcg atc cca acc gaa ctg ccg ggc gta gac acg aag att ctc gat ccg   1488
Ala Ile Pro Thr Glu Leu Pro Gly Val Asp Thr Lys Ile Leu Asp Pro
                485                 490                 495

cgt aac acc tac gct tct ccg gaa cag tgg cag gaa aaa gcc gaa acc   1536
Arg Asn Thr Tyr Ala Ser Pro Glu Gln Trp Gln Glu Lys Ala Glu Thr
            500                 505                 510

ctg gcg aaa ctg ttt atc gac aac ttc gat aaa tac acc gac acc cct   1584
Leu Ala Lys Leu Phe Ile Asp Asn Phe Asp Lys Tyr Thr Asp Thr Pro
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<213> Escherichia coli

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Ile Ser Asp Val His Asp Ile Val Tyr Asn Pro Ser Tyr Asp Leu Leu
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Tyr Gln Glu Glu Leu Asp Pro Ser Leu Thr Gly Tyr Glu Arg Gly Val
35 40 45

Leu Thr Asn Leu Gly Ala Val Ala Val Asp Thr Gly Ile Phe Thr Gly
50 55 60

Arg Ser Pro Lys Asp Lys Tyr Ile Val Arg Asp Asp Thr Thr Arg Asp
65 70 75 80

Thr Phe Trp Trp Ala Asp Lys Gly Lys Gly Lys Asn Asp Asn Lys Pro
85 90 95

Leu Ser Pro Glu Thr Trp Gln His Leu Lys Gly Leu Val Thr Arg Gln
100 105 110

Leu Ser Gly Lys Arg Leu Phe Val Val Asp Ala Phe Cys Gly Ala Asn
115 120 125

Pro Asp Thr Arg Leu Ser Val Arg Phe Ile Thr Glu Val Ala Trp Gln
130 135 140

Ala His Phe Val Lys Asn Met Phe Ile Arg Pro Ser Asp Glu Glu Leu
145 150 155 160

Ala Gly Phe Lys Pro Asp Phe Ile Val Met Asn Gly Ala Lys Cys Thr
165 170 175

Asn Pro Gln Trp Lys Glu Gln Gly Leu Asn Ser Glu Asn Phe Val Ala
180 185 190

Phe Asn Leu Thr Glu Arg Met Gln Leu Ile Gly Gly Thr Trp Tyr Gly
195 200 205

Gly Glu Met Lys Lys Gly Met Phe Ser Met Met Asn Tyr Leu Leu Pro
210 215 220

Leu Lys Gly Ile Ala Ser Met His Cys Ser Ala Asn Val Gly Glu Lys
225 230 235 240

Gly Asp Val Ala Val Phe Phe Gly Leu Ser Gly Thr Gly Lys Thr Thr
245 250 255

Leu Ser Thr Asp Pro Lys Arg Arg Leu Ile Gly Asp Asp Glu His Gly
260 265 270

Trp Asp Asp Asp Gly Val Phe Asn Phe Glu Gly Gly Cys Tyr Ala Lys
275 280 285

Thr Ile Lys Leu Ser Lys Glu Ala Glu Pro Glu Ile Tyr Asn Ala Ile
290 295 300

Arg Arg Asp Ala Leu Leu Glu Asn Val Thr Val Arg Glu Asp Gly Thr
305 310 315 320

Ile Asp Phe Asp Asp Gly Ser Lys Thr Glu Asn Thr Arg Val Ser Tyr
325 330 335

Pro Ile Tyr His Ile Asp Asn Ile Val Lys Pro Val Ser Lys Ala Gly
340 345 350

His Ala Thr Lys Val Ile Phe Leu Thr Ala Asp Ala Phe Gly Val Leu
355 360 365

Pro Pro Val Ser Arg Leu Thr Ala Asp Gln Thr Gln Tyr His Phe Leu
370 375 380

Ser Gly Phe Thr Ala Lys Leu Ala Gly Thr Glu Arg Gly Ile Thr Glu
385 390 395 400

Pro Thr Pro Thr Phe Ser Ala Cys Phe Gly Ala Ala Phe Leu Ser Leu
405 410 415

His Pro Thr Gln Tyr Ala Glu Val Leu Val Lys Arg Met Gln Ala Ala
420 425 430

Gly Ala Gln Ala Tyr Leu Val Asn Thr Gly Trp Asn Gly Thr Gly Lys
435 440 445

Arg Ile Ser Ile Lys Asp Thr Arg Ala Ile Ile Asp Ala Ile Leu Asn
450 455 460

Gly Ser Leu Asp Asn Ala Glu Thr Phe Thr Leu Pro Met Phe Asn Leu
465 470 475 480

Ala Ile Pro Thr Glu Leu Pro Gly Val Asp Thr Lys Ile Leu Asp Pro
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Arg Asn Thr Tyr Ala Ser Pro Glu Gln Trp Gln Glu Lys Ala Glu Thr
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<223> Mutagene DNA

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<222> (1)..(35)
<223> Technical DNA/residues of the polylinker sequence

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<222> (36)..(522)
<223> Part of the 5' region (pck1) of the pckA gene

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<222> (523)..(542)
<223> Technical DNA/residues of the polylinker sequence

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<222> (1106)..(1156)
<223> Technical DNA/residues of the polylinker sequence

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caccaaaaga taagtatatc gtccgtgacg ataccactcg cgatactttc tggtgggcag 180
acaaaggcaa aggtaagaac gacaacaaac ctctctctcc ggaaacctgg cagcatctga 240
aaggcctggt gaccaggcag ctttccggca aacgtctgtt cgttgtcgac gctttctgtg 300
gtgcgaaccc ggatactcgt ctttccgtcc gtttcatcac cgaagtggcc tggcaggcgc 360
attttgtcaa aaacatgttt attcgcccga gcgatgaaga actggcaggt ttcaaaccag 420
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<210> 4
<211> 1294
<212> DNA
<213> Escherichia coli

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<222> (1)..(3)
<223> Start codon of the delta pckA allele

<220>
<221> misc_feature
<222> (1)..(598)
<223> 5' region of the delta pckA allele

<220>
<221> misc_feature
<222> (599)..(618)
<223> Technical DNA/residues of the polylinker sequence

<220>
<221> misc_feature
<222> (619)..(1291)
<223> 3' region of the delta pckA allele

<220>
<221> misc_feature
<222> (1292)..(1294)
<223> Stop codon of the delta pckA allele

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ctgacaggtt atgagcgcgg ggtgttaact aatctgggtg ccgttgccgt cgataccggg 180
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gtggcctggc aggcgcattt tgtcaaaaac atgtttattc gcccgagcga tgaagaactg 480
gcaggtttca aaccagactt tatcgttatg aacggcgcga agtgcactaa cccgcagtgg 540
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<212> DNA

<213> Escherichia coli

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<223> ORF ytfP

<220>
<221> gene
<222> (461)..(727)
<223> ORF yjfA

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<210> 6
<211> 911
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<213> Escherichia coli

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<222> (1)..(383)
<223> 5' flank of the ytfP-yjfA region

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<221> misc_feature
<222> (384)..(911)
<223> 3' flank of the ytfP-yjfA region

<220>
<221> misc_feature

<222> (376)..(378)
<223> ATG codon of the truncated ORF ytfP

<220>
<221> misc_feature
<222> (388)..(390)
<223> ATG codon of the truncated ORF yjfA

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tcagagcgac agtgcggcaa tgacctcgat gctgattggt ttgggggttg cgcaaagtgg 120
ccagattgtg ggtaaaatcg gcgagacgtt tggcgtaagc aatttagcgc tcgacaccca 180
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acacccatct ccaggcgcta ctcgcttgat gaactgctgg cacagtgtga catgaacgcc 780
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<210> 7
<211> 1158
<212> DNA
<213> Escherichia coli

<220>
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<223> Deletion-carrying ytfP-yjfA region

<220>
<221> misc_feature
<222> (1)..(630)
<223> 5' flank of the ytfP-yjfA region

<220>
<221> misc_feature
<222> (631)..(1158)
<223> 3' flank of the ytfP-yjfA region

<220>
<221> misc_feature
<222> (376)..(378)
<223> ATG codon of the truncated ORF ytfP

<220>
<221> misc_feature
<222> (635)..(637)
<223> ATG codon of the truncated ORF yjfA

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ccagattgtg ggtaaaatcg gcgagacgtt tggcgtaagc aatttagcgc tcgacaccca 180
gggagtaggc gactcctccc aggtagtggt cagcggctat gtattgccag gtctgcaagt 240
gaaatacggc gtgggtatat ttgactctat agcaacactc acgttacgtt atcgcctgat 300
gcctaagcta tatctggaag ccgtgtctgg tgtagaccag gcactggatt tgctctatca 360
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tacgcgcgcc agttgattca gacgccgtac tatgcatacg ccaccttcgg gtggcgttgt 660
tttttgcgag acgactcgca ttctgttttg taattccctc accttttgct tttctctccg 720
agccgctttc catatctatt aacgcataaa aaactctgct ggcattcaca aatgcgcagg 780
ggtaaaacgt ttcctgtagc accgtgagtt atactttgta taacttaagg aggtgcagat 840
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<210> 8
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of the Artificial Sequence: Primer pckA'5'-1

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<210> 9
<211> 20
<212> DNA
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<220>
<223> Description of the Artificial Sequence: Primer pckA'5'-2

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<210> 10
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of the Artificial Sequence: Primer pckA'3'-1

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<210> 11
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